

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 24, 2006, 11:23:16 ; Search time 102 Seconds  
(without alignments)  
1620.718 Million cell updates/sec

Title: US-10-783-297A-3  
Perfect score: 93  
Sequence: 1 tgaagcgacccgggtgcc.....tcattctctctctgcagg 93

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues  
Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:\*

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4: /cgn2\_6/ptodata/1/ina/6B COMB.seq:\*

5: /cgn2\_6/ptodata/1/ina/H COMB.seq:\*

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7: /cgn2\_6/ptodata/1/ina/PP COMB.seq:\*

8: /cgn2\_6/ptodata/1/ina/RE COMB.seq:\*

9: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	82	88.2	1001	3	US-09-641-638-320
2	82	88.2	1001	3	US-10-170-097-320
3	82	88.2	26103	3	US-09-949-016-15685
4	82	88.2	26105	3	US-09-949-016-11879
5	36.6	39.4	1899	3	US-09-919-060-15
6	36.6	39.4	1899	3	US-09-919-060-16
7	36.6	39.4	2693	3	US-09-919-060-12
8	36.6	39.4	2693	3	US-09-919-060-14
9	28.4	30.5	601	3	US-09-949-016-54781
10	28.4	30.5	601	3	US-09-949-016-54782
11	28.4	30.5	601	3	US-09-949-016-54783
12	28.4	30.5	24942	3	US-09-949-016-13318
13	28	30.1	1131	3	US-09-902-540-7216
14	28	30.1	4410	3	US-09-902-540-673
15	27.8	29.9	162025	3	US-09-834-700-13
16	27.8	29.9	162025	3	US-09-834-700-14
17	27.8	29.9	162025	3	US-09-834-700-17
18	27.8	29.9	162025	3	US-09-834-700-18
19	27.4	29.5	218	3	US-09-540-236-21
20	27.4	29.5	2531	2	US-08-299-849B-13
21	27.4	29.5	2531	2	US-08-299-849B-14
22	27.4	29.5	2531	2	US-08-142-368A-13
23	27.4	29.5	2531	2	US-08-142-368A-14
24	27.4	29.5	2531	3	US-08-967-727-13

C 25	27.4	29.5	2531	3	US-08-967-727-14	Sequence 14, Appl
C 26	27.4	29.5	2531	3	US-08-037-230D-13	Sequence 13, Appl
C 27	27.4	29.5	2531	3	US-08-037-230D-14	Sequence 14, Appl
C 28	27.4	29.5	2531	3	US-09-583-850-13	Sequence 13, Appl
C 29	27.4	29.5	2531	3	US-09-583-850-14	Sequence 14, Appl
C 30	27.4	29.5	2531	3	US-09-579-197-13	Sequence 13, Appl
C 31	27.4	29.5	2531	3	US-09-579-197-14	Sequence 14, Appl
C 32	27.4	29.5	2531	3	US-09-404-026-13	Sequence 13, Appl
C 33	27.4	29.5	2531	3	US-09-404-026-14	Sequence 14, Appl
C 34	27.4	29.5	2531	3	US-09-312-464-13	Sequence 13, Appl
C 35	27.4	29.5	2531	3	US-09-312-464-14	Sequence 14, Appl
C 36	27.4	29.5	2531	3	US-09-583-848A-13	Sequence 13, Appl
C 37	27.4	29.5	2531	3	US-09-583-848A-14	Sequence 14, Appl
C 38	27.4	29.5	4895	3	US-09-056-105-10	Sequence 10, Appl
C 39	27.4	29.5	11495	3	US-09-056-105-9	Sequence 9, Appl
C 40	27	29.0	1841	3	US-09-050-516-3	Sequence 3, Appl
C 41	27	29.0	1841	3	US-10-278-547-3	Sequence 3, Appl
C 42	27	29.0	2894	3	US-09-050-516-27	Sequence 27, Appl
C 43	27	29.0	2894	3	US-10-278-547-27	Sequence 27, Appl
C 44	26.8	28.8	601	3	US-09-949-016-18615	Sequence 18615, A
C 45	26.8	28.8	601	3	US-09-949-016-134770	Sequence 134770, A

ALIGNMENTS

RESULT 1

US-09-641-638-320  
; Sequence 320, Application US/09641638  
; Patent No. 6432648  
; GENERAL INFORMATION:  
; APPLICANT: Blumenfeld, Marta  
; APPLICANT: Bougueleret, Lydie  
; APPLICANT: Chumakov, Ilya  
; APPLICANT: Cohen, Amick  
; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING  
; FILE REFERENCE: GENSET.051CPI  
; CURRENT APPLICATION NUMBER: US/09/641,638  
; CURRENT FILING DATE: 2000-08-16  
; PRIOR APPLICATION NUMBER: US 09/502,330  
; PRIOR FILING DATE: 2000-02-11  
; PRIOR APPLICATION NUMBER: US 60/133,200  
; PRIOR FILING DATE: 1999-05-07  
; PRIOR APPLICATION NUMBER: US 09/275,267  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: US 60/119,917  
; PRIOR FILING DATE: 1999-02-12  
; NUMBER OF SEQ ID NOS: 1304  
; SOFTWARE: Patent.pm  
; SEQ ID NO 320  
; LENGTH: 1001  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 501  
; OTHER INFORMATION: 10-308-116 : polymorphic base C or T  
; NAME/KEY: misc binding  
; LOCATION: 481..500  
; OTHER INFORMATION: 10-308-116.mis1, potential  
; NAME/KEY: misc binding  
; LOCATION: 502..521  
; OTHER INFORMATION: 10-308-116.mis2, potential complement  
; NAME/KEY: primer bind  
; LOCATION: 386..403  
; OTHER INFORMATION: upstream amplification primer  
; NAME/KEY: primer bind  
; LOCATION: 754..771  
; OTHER INFORMATION: downstream amplification primer, complement  
; NAME/KEY: misc binding  
; LOCATION: 489..513  
; OTHER INFORMATION: 10-308-116 potential probe

US-09-641-638-320

Query Match 88.2%; Score 82; DB 3; Length 1001;  
Best Local Similarity 98.9%; Pred. No. 3.2e-18;  
Matches 93; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 TGAGTGGACCCCGGTCGCCGGTGGGGAATTTCTTGGCTCTCTGCGAGCCTTGAATG 60  
DB 394 TGAGTGGACCCCGGTCGCCGGTGGGGAATTTCTTGGCTCTCTGCGAGCCTTGAATG 453  
QY 61 CCA-GCTCAGCCCTCATCTCTCTCTCTGCGAGG 93  
DB 454 CCAGGCTCAGCCCTCATCTCTCTCTCTGCGAGG 487

RESULT 2

US-10-170-097-320  
Sequence 320, Application US/10170097  
Patent No. 6794143

GENERAL INFORMATION:

APPLICANT: Blumenfeld, Marta  
APPLICANT: Bougueleret, Lydie  
APPLICANT: Chumakov, Ilya  
APPLICANT: Cohen, Annick  
TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING  
FILE REFERENCE: GEN-T114XC2D1  
CURRENT APPLICATION NUMBER: US 09/641,638  
CURRENT FILING DATE: 2002-06-10  
PRIOR FILING DATE: 2000-08-16  
PRIOR APPLICATION NUMBER: US 09/502,330  
PRIOR FILING DATE: 2000-02-11  
PRIOR APPLICATION NUMBER: US 60/133,200  
PRIOR FILING DATE: 1999-05-07  
PRIOR APPLICATION NUMBER: US 09/275,267  
PRIOR FILING DATE: 1999-03-23  
PRIOR APPLICATION NUMBER: US 60/119,917  
PRIOR FILING DATE: 1999-02-12  
NUMBER OF SEQ ID NOS: 1304  
SOFTWARE: Patent.pm  
SEQ ID NO 320  
LENGTH: 1001  
TYPE: DNA  
ORGANISM: Homo Sapiens  
FEATURE:  
NAME/KEY: allele  
LOCATION: 501  
OTHER INFORMATION: 10-308-116 : polymorphic base C or T  
FEATURE:  
NAME/KEY: misc\_binding  
LOCATION: 481..500  
OTHER INFORMATION: 10-308-116.mis1, potential  
FEATURE:  
NAME/KEY: misc\_binding  
LOCATION: 502..521  
OTHER INFORMATION: 10-308-116.mis2, potential complement  
FEATURE:  
NAME/KEY: primer\_bind  
LOCATION: 386..403  
OTHER INFORMATION: upstream amplification primer  
FEATURE:  
NAME/KEY: primer\_bind  
LOCATION: 754..771  
OTHER INFORMATION: downstream amplification primer, complement  
FEATURE:  
NAME/KEY: misc\_binding  
LOCATION: 489..513  
OTHER INFORMATION: 10-308-116 potential probe  
US-10-170-097-320

Query Match 88.2%; Score 82; DB 3; Length 1001;  
Best Local Similarity 98.9%; Pred. No. 3.2e-18;

Matches 93; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 TGAGTGGACCCCGGTCGCCGGTGGGGAATTTCTTGGCTCTCTGCGAGCCTTGAATG 60  
DB 394 TGAGTGGACCCCGGTCGCCGGTGGGGAATTTCTTGGCTCTCTGCGAGCCTTGAATG 453  
QY 61 CCA-GCTCAGCCCTCATCTCTCTCTCTGCGAGG 93  
DB 454 CCAGGCTCAGCCCTCATCTCTCTCTCTGCGAGG 487

RESULT 3

US-09-949-016-15685  
Sequence 15685, Application US/09949016  
Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 15685  
LENGTH: 26103  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-15685

Query Match 88.2%; Score 82; DB 3; Length 26103;  
Best Local Similarity 98.9%; Pred. No. 6.8e-18;  
Matches 93; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 TGAGTGGACCCCGGTCGCCGGTGGGGAATTTCTTGGCTCTCTGCGAGCCTTGAATG 60  
DB 1908 TGAGTGGACCCCGGTCGCCGGTGGGGAATTTCTTGGCTCTCTGCGAGCCTTGAATG 1967  
QY 61 CCA-GCTCAGCCCTCATCTCTCTCTCTGCGAGG 93  
DB 1968 CCAGGCTCAGCCCTCATCTCTCTCTCTGCGAGG 2001

RESULT 4

US-09-949-016-11879  
Sequence 11879, Application US/09949016  
Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED,  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 11879  
LENGTH: 26105  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-11879

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Query Match      88.2%; Score 82; DB 3; Length 26105;
Best Local Similarity 98.9%; Pred. No. 6.8e-18;
Matches: 93; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY      1  TGAATGCGACCCCGGTGCGCGGTGGGGAATTTCTTGGGCTCTCTGTGGAGCCTTGAATG 60
Ddb     1910 TGAATGCGACCCCGGTGCGCGGTGGGGAATTTCTTGGGCTCTCTGTGGAGCCTTGAATG 1969

QY      61 CCA-GCTGAGCCCTCATCTCTCTCTCTCGAGG 93
Ddb     1970 CCAGGCTGAGCCCTCATCTCTCTCTCTCGAGG 2003

RESULT 5
US-09-919-060-15
; Sequence 15, Application US/09919060
; Patent No. 6638744
; GENERAL INFORMATION:
; APPLICANT: Wisniewski, Nancy
; APPLICANT: Brandt, Kevin S.
; TITLE OF INVENTION: CANINE COX-1 AND COX-2 NUCLEIC ACID MOLECULES, PROTEINS AND USES
; FILE REFERENCE: AD-1
; CURRENT APPLICATION NUMBER: US/09/919,060
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/224,486
; PRIOR FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 15
; LENGTH: 1899
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-919-060-15

Query Match      90.4%; Score 36.6; DB 3; Length 1899;
Best Local Similarity 78.3%; Pred. No. 0.0089;
Matches 45; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY      26 GGAATTTCTTGGCTCTCTGTGAGCCTTGAATGCCAGCTCAGCCCTCATCTCTCTC 84
Ddb     32  GGAACCTCTTGGCTCTCTGGGGAGGCTCGAATGCCAGGCCAGCCCTCACTCTCGC 90

RESULT 6
US-09-919-060-16/c
; Sequence 16, Application US/09919060
; Patent No. 6638744
; GENERAL INFORMATION:
; APPLICANT: Wisniewski, Nancy
; APPLICANT: Brandt, Kevin S.
; TITLE OF INVENTION: CANINE COX-1 AND COX-2 NUCLEIC ACID MOLECULES, PROTEINS AND USES
; FILE REFERENCE: AD-1
; CURRENT APPLICATION NUMBER: US/09/919,060
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/224,486
; PRIOR FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 16
; LENGTH: 1899
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-919-060-16

Query Match      39.4%; Score 36.6; DB 3; Length 1899;
Best Local Similarity 76.3%; Pred. No. 0.0089;
Matches 45; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY      26  GGAATTTCTTGGCTCTCTGTGAGCCTTGAATGCCAGCTCAGCCCTCATCTCTCTC 84
Ddb     1868 GGAACCTCTTGGCTCTCTGGGGAGGCTCGAATGCCAGGCCAGCCCTCACTCTCGC 1810

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Db 4 ECDPGARWGIFLASWWSLEQSPSSLSAG 34  
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RESULT 3  
US-10-260-937-63  
; Sequence 63, Application US/10260937  
; Publication No. US20030220306A1  
; GENERAL INFORMATION:  
; APPLICANT: Simmons, Daniel  
; APPLICANT: Chandrasekharan, N. Vishvanath  
; TITLE OF INVENTION: NOVEL CYCLOOXYGENASE VARIANTS AND  
; FILE REFERENCE: 07913-007001  
; CURRENT APPLICATION NUMBER: US/10/260,937  
; CURRENT FILING DATE: 2002-09-28  
; PRIOR FILING DATE: 2001-09-28  
; PRIOR APPLICATION NUMBER: US 60/326,133  
; PRIOR FILING DATE: 2002-04-15  
; PRIOR APPLICATION NUMBER: US 60/373,661  
; PRIOR FILING DATE: 2002-04-16  
; PRIOR APPLICATION NUMBER: US 60/411,575  
; NUMBER OF SEQ ID NOS: 89  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 63  
; LENGTH: 31  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-260-937-63

Query Match 96.6%; Score 169; DB 4; Length 31;  
Best Local Similarity 100.0%; Pred. No. 9.6e-15;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ECDPGARWGIFLASWWSLEQSPSSLSA 30  
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DB 2 ECDPGARWGIFLASWWSLEQSPSSLSA 31  
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RESULT 4  
US-10-260-937-14  
; Sequence 14, Application US/10260937  
; Publication No. US20030220306A1  
; GENERAL INFORMATION:  
; APPLICANT: Simmons, Daniel  
; APPLICANT: Chandrasekharan, N. Vishvanath  
; TITLE OF INVENTION: NOVEL CYCLOOXYGENASE VARIANTS AND  
; FILE REFERENCE: 07913-007001  
; CURRENT APPLICATION NUMBER: US/10/260,937  
; CURRENT FILING DATE: 2002-09-28  
; PRIOR FILING DATE: 2001-09-28  
; PRIOR APPLICATION NUMBER: US 60/326,133  
; PRIOR FILING DATE: 2002-04-15  
; PRIOR APPLICATION NUMBER: US 60/373,661  
; PRIOR FILING DATE: 2002-04-16  
; PRIOR APPLICATION NUMBER: US 60/411,575  
; NUMBER OF SEQ ID NOS: 89  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 613  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-260-937-14

Query Match 77.7%; Score 136; DB 4; Length 613;  
Best Local Similarity 91.7%; Pred. No. 3.2e-09;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ECDPGARWGIFLASWWSLEQQLSP 24  
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DB 4 ECDPGARWGIFLASWWSLEQQLSP 27  
|||||

RESULT 5  
US-10-783-297A-6  
; Sequence 6, Application US/10783297A  
; Publication No. US20040235017A1  
; GENERAL INFORMATION:  
; APPLICANT: Johnson & Johnson Pharmaceutical Research and development  
; TITLE OF INVENTION: HUMAN CYCLOOXYGENASE-3 AND USES THEREOF  
; FILE REFERENCE: PRD-2041  
; CURRENT APPLICATION NUMBER: US/10/783,297A  
; CURRENT FILING DATE: 2004-02-20  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 6  
; LENGTH: 31  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-783-297A-6

Query Match 73.1%; Score 128; DB 5; Length 31;  
Best Local Similarity 80.6%; Pred. No. 2.1e-09;  
Matches 25; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 ECDPGARWGIFLASWWSLEQSPSSLSAG 31  
|||||  
DB 1 ECDPGARWGIFLASGGALNARLSPSSLSAG 31  
|||||

RESULT 6  
US-10-783-297A-11  
; Sequence 11, Application US/10783297A  
; Publication No. US20040235017A1  
; GENERAL INFORMATION:  
; APPLICANT: Johnson & Johnson Pharmaceutical Research and development  
; TITLE OF INVENTION: HUMAN CYCLOOXYGENASE-3 AND USES THEREOF  
; FILE REFERENCE: PRD-2041  
; CURRENT APPLICATION NUMBER: US/10/783,297A  
; CURRENT FILING DATE: 2004-02-20  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 11  
; LENGTH: 630  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-783-297A-11

Query Match 73.1%; Score 128; DB 5; Length 630;  
Best Local Similarity 80.6%; Pred. No. 3.7e-08;  
Matches 25; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 ECDPGARWGIFLASWWSLEQSPSSLSAG 31  
|||||  
DB 4 ECDPGARWGIFLASGGALNARLSPSSLSAG 34  
|||||

RESULT 7  
US-10-437-963-105915  
; Sequence 105915, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

GenCore version 5.1.6  
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QM nucleic - nucleic search, using sw model

Run on: January 24, 2006, 11:03:01 ; Search time 1749 Seconds  
(without alignments)  
3022.551 Million cell updates/sec

Title: US-10-783-297A-3

Perfect score: 93

Sequence: 1 tgatcgagcccggtgcc.....tcattctctctctgcagg 93

Scoring table: IDENTITY\_NUC

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Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pr.\*

9: gb\_ro.\*

10: gb\_sts.\*

11: gb\_sy.\*

12: gb\_un.\*

13: gb\_vl.\*

14: gb\_btg.\*

15: gb\_pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	93	100.0	93	6	CQ869567	CQ869567 Sequence
2	93	100.0	1238	8	HUMPROHSYN	L08404 Homo sapien
3	93	100.0	1893	6	CQ869572	CQ869572 Sequence
4	82	88.2	1001	6	AR582395	AR582395 Sequence
5	82	88.2	26782	8	AF440204	AF440204 Homo sapi
6	82	88.2	28670	8	AY449688	AY449688 Homo sapi
7	82	88.2	19985	14	AL353767	AL353767 Homo sapi
8	82	88.2	223020	8	AL162424	AL162424 Human DNA
9	81	87.1	94	8	AY884200	AY884200 Homo sapi
10	70	75.3	93	6	CQ869569	CQ869569 Sequence
11	70	75.3	1860	6	CQ869574	CQ869574 Sequence
12	44.8	48.2	10377	6	AX347123	AX347123 Sequence
13	42	45.2	10377	6	AX347122	AX347122 Sequence
14	38	40.9	38	6	CQ869578	CQ869578 Sequence
15	36.6	39.4	1899	6	AR411937	AR411937 Sequence
16	36.6	39.4	1899	6	AR411938	AR411938 Sequence
17	36.6	39.4	1901	4	AF535139	AF535139 Canis fam
18	36.6	39.4	2693	6	AR411935	AR411935 Sequence

C	19	36.6	39.4	2693	6	AR411936	AR411936 Sequence
	20	36.6	39.4	2706	4	AF535138	AF535138 Canis fam
	21	34.4	37.0	187858	9	AC153542	AC153542 Mus muscu
C	22	32.8	35.3	210956	14	AC162366	AC162366 Mus muscu
	23	32.8	35.3	258003	14	AC122205	AC122205 Mus muscu
C	24	32.4	34.8	258484	14	AC125555	AC125555 Rattus no
C	25	31.6	34.0	110000	14	CT005269_03	Continuation (4 of
C	26	31.4	33.8	100000	8	AP000077	AP000077 Homo sapi
	27	31.4	33.8	156296	8	AP006205	AP006205 Homo sapi
	28	31.4	33.8	157665	8	AP006205	AP006205 Homo sapi
	29	31.4	33.8	170261	8	AC090809	AC090809 Homo sapi
C	30	31	33.3	235097	14	AC159664	AC159664 Bos tauru
	31	30.6	32.9	89936	15	AP004532	AP004532 Lotu cor
	32	30.6	32.9	175388	8	AC116664	AC116664 Papio ham
C	33	30.2	32.5	134156	8	AL357083	AL357083 Human DNA
C	34	30.2	32.5	178145	8	AC018659	AC018659 Homo sapi
C	35	30.2	32.5	224571	14	AC159850	AC159850 Bos tauru
	36	30	32.3	1296	5	AF077092	AF077092 Gallus ga
	37	30	32.3	1394	5	EX935055	EX935055 Gallus ga
C	38	30	32.3	1802	5	AF076640	AF076640 Gallus ga
C	39	30	32.3	143392	15	AC149299	AC149299 Populus t
C	40	30	32.3	231140	14	AC098904	AC098904 Rattus no
C	41	29.6	31.8	140031	14	AC121686	AC121686 Rattus no
C	42	29.6	31.8	161179	14	AC066601	AC066601 Homo sapi
C	43	29.6	31.8	171296	8	CNS06C86	AL391262 Human chr
	44	29.6	31.8	189332	14	AC155501	AC155501 Zea mays
C	45	29.6	31.8	231198	14	AC126892	AC126892 Rattus no

ALIGNMENTS

RESULT 1  
LOCUS CQ869567 93 bp DNA linear PAT 13-SEP-2004  
DEFINITION Sequence 3 from Patent WO2004074311.  
ACCESSION CQ869567  
VERSION CQ869567.1 GI:51999447

KEYWORDS Homo sapiens (human)

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE 1

Qin, N., Flores, C., Zhang, S. P. and Codd, G. E.

Human cyclooxygenase-3 and uses thereof

Patent: WO 2004074311-A 3 02-SEP-2004;

JANSSEN PHARMACEUTICA N.V. (BE)

Location/Qualifiers

source 1 93

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

ORIGIN

Query Match

Best Local Similarity

Matches

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0; Mismatches

0; Indels

0; Gaps

0;

Qy

1 TGAGTGGGACCCCGGTCGCGGAGATTTCTTGGCCCTCTCTGAGCCTTGAATG 60

Db

1 TGAGTGGGACCCCGGTCGCGGAGATTTCTTGGCCCTCTCTGAGCCTTGAATG 60

Qy

61 CCAGCTCAGCCCTCATCTCTCTCTGAGG 93

Db

61 CCAGCTCAGCCCTCATCTCTCTCTGAGG 93

RESULT 2

HUMPROHSYN

LOCUS

DEFINITION

Homo sapiens prostaglandin H synthase 1 gene, complete promoter.

1238 bp DNA linear PRI 27-APR-1993

ACCESSION L08404  
 VERSION L08404.1 GI:190413  
 KEYWORDS prostaglandin H synthase 1.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominiidae; Homo.  
 REFERENCE 1 (bases 1 to 1238)  
 AUTHORS Wang, L.H., Hajibeigi, A., Xu, X.M., Loose-Mitchell, D. and Wu, K.K.  
 TITLE Characterization of the promoter of human prostaglandin H synthase-1 gene  
 JOURNAL Biochem. Biophys. Res. Commun. 190 (2), 406-411 (1993)  
 PUBMED 8427584  
 COMMENT Original source text: Homo sapiens (library: pWE15 cosmid genomic) male DNA.  
 FEATURES  
 source Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /sex="male"  
 /cell\_type="lymphocyte"  
 /tissue\_lib="pWE15 cosmid genomic"  
 899..1040  
 promoter  
 899..906  
 intron  
 1041..1133  
 exon  
 1134..1220  
 exon  
 ORIGIN  
 Query Match 100.0%; Score 93; DB 8; Length 1238;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-19;  
 Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TGAGTGGACCCCGGTCGGGGAATTTCTTGGCTCTCTCTGAGCCTTGAATG 60  
 DB 1042 TGAGTGGACCCCGGTCGGGGAATTTCTTGGCTCTCTCTGAGCCTTGAATG 1101  
 QY 61 CCAGCTCAGCCCTCATCTCTCTCTCTGAGG 93  
 DB 1102 CCAGCTCAGCCCTCATCTCTCTCTCTGAGG 1134  
 RESULT 3  
 LOCUS C0869572 1893 bp DNA linear PAT 13-SEP-2004  
 DEFINITION Sequence 8 from Patent WO2004074311.  
 ACCESSION C0869572  
 VERSION C0869572.1 GI:51999450  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominiidae; Homo.  
 REFERENCE 1  
 AUTHORS Qin, N., Flores, C., Zhang, S.P. and Codd, G.E.  
 TITLE Human cyclooxygenase-3 and uses thereof  
 JOURNAL Patent: WO 2004074311-A 8 02-SEP-2004;  
 JANSSEN PHARMACEUTICA N.V. (BE)  
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 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
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 Query Match 100.0%; Score 93; DB 6; Length 1893;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-19;  
 Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TGAGTGGACCCCGGTCGGGGAATTTCTTGGCTCTCTCTGAGCCTTGAATG 60  
 DB 1042 TGAGTGGACCCCGGTCGGGGAATTTCTTGGCTCTCTCTGAGCCTTGAATG 1101  
 QY 61 CCAGCTCAGCCCTCATCTCTCTCTCTGAGG 93  
 DB 1102 CCAGCTCAGCCCTCATCTCTCTCTCTGAGG 1134

DB 9 TGAGTGGACCCCGGTCGGGGAATTTCTTGGCTCTCTCTGAGCCTTGAATG 68  
 QY 61 CCAGCTCAGCCCTCATCTCTCTCTCTGAGG 93  
 DB 69 CCAGCTCAGCCCTCATCTCTCTCTCTGAGG 101  
 RESULT 4  
 LOCUS AR582395 1001 bp DNA linear PAT 15-DEC-2004  
 DEFINITION Sequence 320 from patent US 6794143.  
 ACCESSION AR582395  
 VERSION AR582395.1 GI:56617764  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 1001)  
 AUTHORS Blumenfeld, M., Bougueleret, L., Chumakov, I. and Cohen, A.  
 TITLE Biallelic markers derived from genomic regions carrying genes involved in arachidonic acid metabolism  
 JOURNAL Patent: US 6794143-A 320 21-SEP-2004;  
 Genset S.A.;  
 FRX;  
 FEATURES  
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 /mol\_type="genomic DNA"  
 ORIGIN  
 Query Match 88.2%; Score 82; DB 6; Length 1001;  
 Best Local Similarity 98.9%; Pred. No. 4.9e-16;  
 Matches 93; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 QY 1 TGAGTGGACCCCGGTCGGGGAATTTCTTGGCTCTCTCTGAGCCTTGAATG 60  
 DB 394 TGAGTGGACCCCGGTCGGGGAATTTCTTGGCTCTCTCTGAGCCTTGAATG 453  
 QY 61 CCA-GCTCAGCCCTCATCTCTCTCTGAGG 93  
 DB 454 CCAGCTCAGCCCTCATCTCTCTCTGAGG 487  
 RESULT 5  
 LOCUS AF440204 26782 bp DNA linear PRI 23-OCT-2002  
 DEFINITION Homo sapiens prostaglandin-endoperoxide synthase 1 (PTGS1) gene, exons 1 through 11 and complete cds.  
 ACCESSION AF440204  
 VERSION AF440204.1 GI:17017286  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominiidae; Homo.  
 REFERENCE 1 (bases 1 to 26782)  
 AUTHORS Scott, B.T., Hastett, S.J., Bovill, E.G., Callas, P.W., Valliere, J.E., Wang, L., Wu, K.K. and Long, G.L.  
 TITLE Characterization of the human prostaglandin H synthase 1 gene (PTGS1): exclusion by genetic linkage analysis as a second modifier gene in familial thrombosis  
 JOURNAL Blood Coagul. Fibrinolysis 13 (6), 519-531 (2002)  
 PUBMED 12192304  
 REFERENCE 2 (bases 1 to 26782)  
 AUTHORS Scott, B.T., Hastett, S.J., Bovill, E.G., Callas, P.W., Valliere, J.E., Wang, L., Wu, K.K. and Long, G.L.  
 TITLE Direct Submission  
 JOURNAL Submitted (25-OCT-2001) Pathology, University of Vermont, Burlington, VT 05403, USA  
 FEATURES  
 source Location/Qualifiers  
 1..26782  
 /organism="Homo sapiens"